

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=10; hr=15; min=2; sec=27; ms=427;]

=====

Application No: 10554387 Version No: 2.0

Input Set:

Output Set:

Started: 2009-02-19 11:43:19.381
Finished: 2009-02-19 11:43:20.363
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 982 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

SEQUENCE LISTING

<110> Protalix Ltd.
 Shaaltiel, Yoseph
 Baum, Gideon
 Hashmueli, Sharon
 Lewkowicz, Ayala
 Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<140> 10554387

<141> 2005-10-25

<150> IL 155588

<151> 2003-04-27

<150> PCT/IL2004/000181

<151> 2004-02-24

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> ER signal peptide

<400> 1

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
 1 5 10 15

Leu Ser Ser Ala Glu Phe
 20

<210> 2

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Vacuolar targeting signal from Tobacco chitinase A

<400> 2

Asp Leu Leu Val Asp Thr Met
 1 5

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 3
 cagaattcgc ccgcccctgc a 21

<210> 4
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 4
 ctcagatctt ggcgatgcca ca 22

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 5
 ctcagaagac cagagggct 19

<210> 6
 <211> 17
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 6
 caaagcggcc atcgtgc 17

<210> 7
 <211> 1491
 <212> DNA
 <213> Homo sapiens

 <400> 7
 gcccgccct gcaccctaa aagcttcggc tacagctcgg tgggtgtgtgt ctgcaatgcc 60

acatactgtg actcctttga cccccgacc tttcctgccc ttggtacctt cagccgctat	120
gagagtacac gcagtgggcg acggatggag ctgagtatgg ggcccatcca ggctaatacac	180
acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga	240
tttgaggagg ccatagacaga tgetgctgct ctcaacatcc ttgccctgtc acccctgcc	300
caaaatttgc tacttaaatac gtactttctct gaagaaggaa tcggatataa catcatccgg	360
gtacccatgg ccagctgtga cttctccatc cgcacctaca cctatgcaga caccctgat	420
gatttccagt tgcacaactt cagcctccca gaggaagata ccaagctcaa gataccctg	480
attcaccgag ccctgcagtt ggcccagcgt cccgtttcac tccttgccag ccctggaca	540
tcacccactt ggctcaagac caatggagcg gtgaatggga aggggtcact caagggacag	600
cccggagaca tctaccacca gacctgggcc agatactttg tgaagtccct ggatgcctat	660
gctgagcaca agttacagtt ctgggcagtg acagctgaaa atgagccttc tgctgggctg	720
ttgagtggat accccttcca gtgcctgggc ttcacccctg aacatcagcg agacttcatt	780
gcccgtgacc taggtcctac cctcgccaac agtactcacc acaatgtccg cctactcatg	840
ctggatgacc aacgcttgct gctgccccac tgggcaaagg tggactgac agaccagaa	900
gcagctaaat atgttcatgg cattgctgta cattggtacc tggactttct ggctccagcc	960
aaagccaccc taggggagac acaccgctg ttccccaaca ccatgctctt tgcctcagag	1020
gcctgtgtgg gctccaagtt ctgggagcag agtgtgcggc taggctcctg ggatcgaggg	1080
atgcagtaca gccacagcat catcacgaac ctctgtacc atgtggtcgg ctggaccgac	1140
tggaaccttg ccctgaaccc cgaaggagga cccaattggg tgcgtaactt tgtcgacagt	1200
cccatcattg tagacatcac caaggacacg ttttacaac agcccatgtt ctaccacctt	1260
ggccacttca gcaagttcat tcctgagggc tcccagagag tggggctggt tgccagtcag	1320
aagaacgacc tggacgcagt ggcactgatg catcccgatg gctctgctgt tgtggtcgtg	1380
ctaaaccgct cctctaagga tgtgcctctt accatcaagg atcctgctgt gggcttcctg	1440
gagacaatct cacctggcta ctccattcac acctacctgt ggcacgcca g	1491

<210> 8
 <211> 496
 <212> PRT
 <213> Homo sapiens

<400> 8

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys

1	5	10	15
Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro	20	25	30
Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg	35	40	45
Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly	50	55	60
Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly	65	70	75
Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu	85	90	95
Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu	100	105	110
Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe	115	120	125
Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu	130	135	140
His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu	145	150	155
Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala	165	170	175
Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn	180	185	190
Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr	195	200	205
Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys	210	215	220
Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu	225	230	235
			240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gly Arg Leu Leu Leu
275 280 285

His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val
290 295 300

His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys
305 310 315 320

Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe
325 330 335

Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg
340 345 350

Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr
355 360 365

Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu
370 375 380

Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro
385 390 395 400

Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe
405 410 415

Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg
420 425 430

Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu
435 440 445

Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser
450 455 460

Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
 465 470 475 480

Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
 485 490 495

<210> 9
 <211> 338
 <212> DNA
 <213> Cauliflower mosaic virus

<400> 9
 ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac 60
 ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120
 ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180
 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240
 tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300
 tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10
 <211> 66
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding the ER signal peptide

<400> 10
 atgaagacta atctttttct ctttctcatc ttttcacttc tcctatcatt atcctcggcc 60
 gaattc 66

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11
 gatcttttag tcgatactat g 21

<210> 12
 <211> 167
 <212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

<220>

<221> misc_feature

<222> (162)..(162)

<223> n is a, c, g, or t

<400> 12

taatttc	atctgtttt	gttattccc	ttgcaatgca	gggcctaggg	ctatgaataa	60
agttaat	gtgtgaat	gtgtgat	gtgacctga	agggatcacg	actataatcg	120
tttataataa	acaaagactt	tgtcccaaaa	accccccccc	cngcaga		167

<210> 13

<211> 2186

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding high mannose human glucocerebrosidase (GCD)

<220>

<221> misc_feature

<222> (2181)..(2181)

<223> n is a, c, g, or t

<400> 13

ttttcacaaa	gggtaatatc	gggaaacctc	ctcggattcc	attgcccagc	tatctgtcac	60
ttcatcgaaa	ggacagtaga	aaaggaaggt	ggctcctaca	aatgccatca	ttgcgataaa	120
ggaaaggcta	tcgttcaaga	tgctcttacc	gacagtggtc	ccaaagatgg	acccccaccc	180
acgaggaaca	tcgtggaaaa	agaagacgtt	ccaaccacgt	cttcaaagca	agtggattga	240
tgtgatattc	ccactgacgt	aagggatgac	gcacaatccc	actatccttc	gcaagaccct	300
tcctctatat	aaggaagttc	atttcatttg	gagaggacag	gcttcttgag	atccttcaac	360
aattaccaac	aacaacaaac	aacaacaaac	attacaatta	ctatttacia	ttacagtcga	420
gggatccaag	gagatataac	aatgaagact	aatctttttc	tctttctcat	cttttcactt	480
ctcctatcat	tatcctcggc	cgaattcgcc	cgcccccgca	tcctaaaaag	cttcgggtac	540
agctcggttg	tgtgtgtctg	caatgccaca	tactgtgact	cctttgaccc	cccgaccttt	600
cctgcccttg	gtaccttcag	ccgctatgag	agtacacgca	gtgggcgacg	gatggagctg	660

agtatggggc ccatccaggc taatcacacg ggcacaggcc tgctactgac cctgcagcca	720
gaacagaagt tccagaaagt gaagggattt ggagggggcca tgacagatgc tgctgctctc	780
aacatccttg cctgtgcacc ccctgcccaa aatttgctac ttaaatacgta cttctctgaa	840
gaaggaatcg gatataacat catccgggta cccatggcca gctgtgactt ctccatccgc	900
acctacacct atgcagacac ccctgatgat ttccagttgc acaacttcag cctcccagag	960
gaagatacca agctcaagat acccctgatt caccgagccc tgcagttggc ccagcgtccc	1020
gtttcactcc ttgccagccc ctggacatca ccacttggc tcaagaccaa tggagcggtg	1080
aatgggaagg ggtcactcaa gggacagccc ggagacatct accaccagac ctggggccaga	1140
tactttgtga agttcctgga tgcctatgct gagcacaagt tacagttctg ggcagtgaca	1200
gctgaaaatg agccttctgc tgggctggtg agtggatacc ccttcagtg cctgggcttc	1260
accctgaac atcagcgaga cttcattgcc cgtgacctag gtcctaccct cgccaacagt	1320
actcaccaca atgtccgct actcatgctg gatgaccaac gcttgcctg gccccactgg	1380
gcaaagggtg tactgacaga cccagaagca gctaaatatg ttcattggcat tgctgtacat	1440
tggtacctgg actttctggc tccagccaaa gccaccctag gggagacaca ccgcctgttc	1500
cccaacacca tgctctttgc ctcagaggcc tgtgtgggct ccaagtctctg ggagcagagt	1560
gtgcggctag gctcctggga tcgagggatg cagtacagcc acagcatcat cacgaacctc	1620
ctgtaccatg tggtcggctg gaccgactgg aaccttgccc tgaaccccgaggaggacccc	1680
aattgggtgc gtaactttgt cgacagtccc atcattgtag acatcaccaa ggacacgttt	1740
tacaaacagc ccatgttcta ccaccttggc cacttcagca agttcattcc tgagggctcc	1800
cagagagtgg ggctggttgc cagtcagaag aacgacctgg acgcagtggc actgatgcat	1860
cccgatggct ctgctgttgt ggtcgtgcta aaccgctcct ctaaggatgt gcctcttacc	1920
atcaaggatc ctgctgtggg ctccctggag acaatctcac ctggctactc cattcacacc	1980
tacctgtggc atcgccaaga tcttttagtc gatactatgt aatttcatga tctgttttgt	2040
tgtattccct tgcaatgcag ggcctagggc tatgaataaa gttaatgtgt gaatgtgtga	2100
atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt	2160
gtcccaaaaa ccccccccc ngcaga	2186

<210> 14

<211> 526

<212> PRT

<213> Artificial sequence

<220>

<223> High mannose human glucocerebrosidase (GCD)

<400> 14

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
1 5 10 15

Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
20 25 30

Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
130 135 140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
145 150 155 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
165 170 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
195 200 205

Thr	Asn	Gly	Ala	Val	Asn	Gly	Lys	Gly	Ser	Leu	Lys	Gly	Gln	Pro	Gly	210	215	220	
Asp	Ile	Tyr	His	Gln	Thr	Trp	Ala	Arg	Tyr	Phe	Val	Lys	Phe	Leu	Asp	225	230	235	240
Ala	Tyr	Ala	Glu	His	Lys	Leu	Gln	Phe	Trp	Ala	Val	Thr	Ala	Glu	Asn	245	250	255	
Glu	Pro	Ser	Ala	Gly	Leu	Leu	Ser	Gly	Tyr	Pro	Phe	Gln	Cys	Leu	Gly	260	265	270	
Phe	Thr	Pro	Glu	His	Gln	Arg	Asp	Phe	Ile	Ala	Arg	Asp	Leu	Gly	Pro	275	280	285	
Thr	Leu	Ala	Asn	Ser	Thr	His	His	Asn	Val	Arg	Leu	Leu	Met	Leu	Asp	290	295	300	
Asp	Gln	Arg	Leu	Leu	Leu	Pro	His	Trp	Ala	Lys	Val	Val	Leu	Thr	Asp	305	310	315	320
Pro	Glu	Ala	Ala	Lys	Tyr	Val	His	Gly	Ile	Ala	Val	His	Trp	Tyr	Leu	325	330	335	
Asp	Phe	Leu	Ala	Pro	Ala	Lys	Ala	Thr	Leu	Gly	Glu	Thr	His	Arg	Leu	340	345	350	
Phe	Pro	Asn	Thr	Met	Leu	Phe	Ala	Ser	Glu	Ala	Cys	Val	Gly	Ser	Lys	355	360	365	
Phe	Trp	Glu	Gln	Ser	Val	Arg	Leu	Gly	Ser	Trp	Asp	Arg	Gly	Met	Gln	370	375	380	
Tyr	Ser	His	Ser	Ile	Ile	Thr	Asn	Leu	Leu	Tyr	His	Val	Val	Gly	Trp	385	390	395	400
Thr	Asp	Trp	Asn	Leu	Ala	Leu	Asn	Pro	Glu	Gly	Gly	Pro	Asn	Trp	Val	405	410	415	
Arg	Asn	Phe	Val	Asp	Ser	Pro	Ile	Ile	Val	Asp	Ile	Thr	Lys	Asp	Thr	420	425	430	

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
435 440 445

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
450 455 460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
465 470 475 480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
485 490 495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
500 505 510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
515 520 525